Enhancing precision oncology for Haitian breast cancer patients through deep learning-enabled computational pathology tools.

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Background: While early-stage breast cancer is often curable in high-resource settings, mortality-to-incidence ratios remain unacceptably high for women in lower- and middle-income countries (LMIC). This disparity is due to an inability within LMICs for patients to access basic cancer diagnostics (e.g., IHC). Consequently, there is a major need to develop innovative approaches for the cancer diagnostic-therapeutic pipeline to deliver high-quality care for LMIC patients. To this end, deep learning (DL) has shown considerable promise in identifying clinically relevant biology within histopathology (H&E). Therefore, we have curated an unprecedented dataset of H&E whole slide images (WSIs) and tissue-matched estrogen receptor (ER) status for 5500 breast cancer slides from Zanmi Lasante (Haiti). **Methods:** Using The Cancer Genome Atlas (TCGA) breast cancer and Haitian datasets, we trained a DL-enabled tool, using H&E WSIs, to predict ER status for each patient. As the TCGA dataset predominantly comprises patients of European ancestry, we assessed whether a TCGA-trained model would generalize to Haitian patients. After WSI processing and feature extraction, attention-based weakly supervised multiple instance learning was used to train a classification model. To assess performance, both the TCGA and Zanmi Lasante datasets were split into training (70%), validation (15%), and testing (15%) sets, and the results were compared across both patient populations. **Results:** Using the TCGA dataset (2100 H&E WSIs), we trained an ER classification model. This model demonstrated a performance of an area under receiver operating characteristic (AUROC) of 0.92 on the "held-out" TCGA test set, but only an AUROC of 0.71 on the Haitian "held-out" test set for ER status prediction. This drop in model performance, or domain shift, is consistent with known biological differences between breast cancers enriched in Black women compared to those in Caucasian women. Notably, pre-training our model on the TCGA dataset and then fine-tuning on a portion of the Haitian training set (2800 WSIs) substantially improved predictive performance to an AUROC of 0.85 on the Haiti test set. **Conclusions:** This study illustrates the potential of DL to advance precision oncology in low-resource settings and highlights the need for adequate training data from LMIC patients. We anticipate tools from this work will be deployed for use in Haitian breast cancer patients to inform precision-based use of endocrine therapies. Research Sponsor: None.